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Supply-Chain Perturbations and Multi-Platform Robustness in Honey Authentication: Implications for Emerging New Zealand Monofloral Honeys

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Abstract

New Zealand monofloral honeys beyond mānuka, including rewarewa and kāmahi, require authentication systems that remain reliable under realistic supply-chain conditions rather than under idealized laboratory settings alone. This review evaluates how three categories of supply-chain perturbation affect authentication-relevant chemical markers. Thermal processing alters volatile and phenolic domains in a marker-specific manner while leaving trace elements comparatively stable. Filtration and ultrafiltration selectively remove pollen and certain non-volatile markers, although the evidence base for ultrafiltration-specific effects remains limited. Syrup adulteration distorts elemental ratios and can be detected through targeted small-molecule markers, but discriminatory power may weaken during post-adulteration storage. A comparative assessment of four analytical platform categories (GC-MS, LC-MS/MS, ICP-MS, and rapid spectroscopic methods) shows that each carries a distinct vulnerability profile and that no single platform provides uniform robustness across all perturbation types. On this basis, this review proposes a Sentinel Stress-Testing Framework for future authentication claims, comprising perturbation-aware challenge tiers, mandatory external validation on independent sample sets, and multi-block data fusion to exploit cross-platform redundancy. This framework provides a transferable basis for future commercial.

Keywords

honey authentication, New Zealand monofloral honey, non-mānuka honey, supply-chain perturbations, data fusion, external validation

1. Introduction

Honey authentication models are often developed and evaluated under idealized laboratory conditions, but the chemical markers these models rely on do not remain stable across the supply chain. Heating attenuates volatile compounds and reshapes phenolic profiles; filtration and ultrafiltration selectively remove pollen and certain non-volatile markers; syrup adulteration dilutes or replaces the original honey matrix. As a result, authentication performance may fail because the marker is altered, removed, or masked once the sample has been processed, stored, or adulterated. Different analytical platforms compound this difficulty, as each interrogates a different chemical domain. A model built on volatile compounds faces a different perturbation risk profile from one built on phenolics, elemental ratios, or bulk spectral signals. The practical question

extends beyond which markers can distinguish botanical origin to the conditions under which those markers remain reliable.

This gap takes on sharper relevance against the backdrop of intensifying international scrutiny. The European Commission's coordinated "From the Hives" action found that 46% of honey samples analyzed were suspected non-compliant [1]. The regulatory response has moved beyond fraud detection. Directive (EU) 2024/1438 now requires the Commission to adopt harmonized methods for detecting adulteration by June 2028 and to establish delegated criteria covering heating, pollen removal, and Union-wide traceability by June 2029. It also mandates the establishment of a formal platform involving Member States, laboratories, and honey industry stakeholders [2]. It means that authenticity claims will be judged not only by whether a honey can be classified under ideal laboratory conditions, but against realistic supply-chain perturbations.

For mānuka, New Zealand has already built one such credibility framework. Honey labeled as mānuka for export must satisfy an MPI-recognized five-attribute definition: four chemical markers (MGO, DHA, leptosperin, 2′-methoxybenzoic acid) and one DNA marker from mānuka pollen [3]. No equivalent framework exists for non-mānuka monofloral honeys. Recent work has identified rewarewa-associated markers, including high aliphatic diacid content and 2-methoxybutanedioic acid, and kāmahi-associated markers, including kamahines A-C and meliracemoic acid [4]. However, the same literature also indicates that the chemical characterization of several New Zealand native honeys remains incomplete, that the origins of some markers are uncertain, and that the reliability of pollen-based identification is limited [4]. The direct literature on rewarewa and kāmahi is still too thin to support a self-contained review. Hence, the framework developed here draws on the broader honey authentication literature to identify transferable principles.

This review does not attempt to compile or extend that marker inventory. The focus is on determining under what conditions these biomarkers can be relied upon once identified. The broader literature shows that botanical origin discrimination has been the most intensively studied authenticity problem, and that chromatographic techniques have been especially prominent, while also emphasizing that honey authenticity remains analytically challenging and in need of continued methodological refinement [5]. Accordingly, this review evaluates how supply chain perturbations affect authentication-relevant markers, how different analytical platforms respond to those perturbations, and why future authentication claims for New Zealand monofloral honeys should be supported by stress testing, external validation, and multi-platform evidence, rather than classification accuracy measured under a single set of controlled conditions.

2. Perturbation Effects on Authentication-Relevant Markers

The chemical markers used for honey authentication are not inherently stable across the supply chain. Between harvest and retail, honey may experience thermal processing, filtration, and deliberate adulteration. Each of these interventions acts on different marker classes. So, a marker that survives one perturbation may be compromised by another. The following subsections examine three perturbations: thermal processing, filtration and ultrafiltration, and syrup adulteration.

2.1 Thermal Processing

Thermal processing is applied during honey extraction, liquefaction, and pasteurization, typically at 50 - 90 °C. These temperatures can cause significant alterations in chemical markers.

Volatile compounds are particularly susceptible. Heating mānuka honey at 90 ℃ significantly attenuated both methylglyoxal (MGO) and 2'-methoxyacetophenone (MAP), two compounds central to mānuka's chemical identity. Furfural and 5-hydroxymethylfurfural (HMF) accumulate as neo-formed thermal artifacts under moderate heating [6, 7].

Certain thermal by-products can serve as indicators of processing. The Amadori compound Fru-Phe exceeded 10 mg/kg in heated acacia honey, compared with less than 1.54 mg/kg in unheated controls, and has been proposed as a thermal history marker [8]. Phenolics respond less predictably. Heating at 60 - 80°C reduces total phenolic content and antioxidant capacity, but flavonoids are more heat-resistant than phenolic acids [7]. By contrast, trace elements appear to be entirely indifferent to heat. Czipa et al. [9] demonstrated that neither thermal processing nor year of collection altered the elemental composition of acacia honey.

The ultimate result is that thermal processing not only degrades the chemical fingerprint of honey but also reshapes it by eliminating certain signals, amplifying others, and introducing artificial interference that may be mistaken for botanical characteristics, particularly when the processing history is unknown. For authentication models, the practical implication is that the thermal processing history itself constitutes an analytical variable.

2.2 Filtration and Ultrafiltration

Filtration and ultrafiltration are standard physical processing steps in honey production. Unlike thermal processing, they do not trigger thermochemical transformations. Instead, they act by selective removal. In honey processing, microfiltration is typically described by pore size, while ultrafiltration is more appropriately defined by molecular weight cut-off (MWCO). Reported UF studies have used membranes with a molecular weight cutoff of 25–100 kDa, which are sufficient to remove yeast cells and reject honey enzymes[10]. This has a direct negative impact on pollen-based authentication. This effect is particularly acute for native New Zealand honeys, such as rewarewa honey. As this plant relies on birds for pollination, bees do not come into contact with pollen during nectar collection, making pollen identification cannot be reliably guaranteed even before filtration [4].

Ultrafiltration also diminishes phenolic markers. Because many phenolic acids and flavonoids in honey are far smaller than UF cut-offs, their depletion is not because of size exclusion alone. Co-retention with proteins, colloidal material, or pollen-derived particles, together with adsorption and dynamic layer formation at the membrane surface, is a more plausible mechanism. After ultrafiltration, protocatechuic acid, abscisic acid, and ellagic acid had been significantly depleted in honeydew honey [11]. It implies that membrane processing can deplete small-molecule markers via matrix-associated retention, thereby preventing them from being fully reflected in the matrix.

Centrifugation and standard filtration also reduced mineral content in acacia honey, although ultrafiltration-specific mineral loss remains poorly quantified [9]. The evidence base for filtration effects on authentication markers is thinner than that for thermal processing or adulteration. Many studies examine filtration as one step within a multi-step processing sequence rather than as an isolated variable, which limits the ability to attribute specific marker changes to a specific filtration treatment.

2.3 Syrup Adulteration

Syrup adulteration is the most widely researched perturbation in the literature on honey authenticity. Rather than degrading existing markers through physical or chemical transformation, adulteration alters the chemical fingerprint by diluting or replacing the original honey matrix with exogenous sugar syrups. These syrups should not be treated as a single class; C4 syrups, such as corn- or cane-derived sweeteners, are analytically distinct from C3 syrups, such as rice or beet, especially in isotope-based authentication. This dilution mechanism produces strong effects on elemental ratios. For C4 adulterants, this matrix shift is complemented by a carbon-isotope contrast; C4 plants typically show δ13C values around -9 to -15‰, whereas C3 plants fall around -23 to -28‰ [12]. Accordingly, classical EA-IRMS can detect C4 syrup addition at ≥7%, but not C3 syrup adulteration. The K/Na ratio decreased by over 90% at 50% beet syrup adulteration and was already shifted at 10% [13].

At the small-molecule level, certain targeted markers are highly sensitive. C3 adulterants isotope signatures overlap more closely with authentic honey and therefore place greater reliance on syrup-specific molecular markers or higher-resolution methods [14]. HPLC-DAD detected the rice syrup marker AFGP at 10%, and LC-MS/MS detected it at 1% [15], and LC-HRMS detected a syrup-specific marker at m/z 515.1444 with a quantification limit of around 5 % [16].

Low-level adulteration under realistic supply-chain conditions presents a different problem. The inherent chemical diversity of natural honeys may overlap with the metabolic patterns of highly processed syrups, narrowing the discriminatory margin [17]. Adulteration markers do not remain stable over time. The disparity between authentic and adulterated NIR signals was greatest immediately after adulteration and diminished within three months [18]. This temporal decay means that samples used to confirm a model through freshly adulterated samples can give false promises of reliability when applied to aged products.

Therefore, the practical challenge is not identifying fresh, obvious fraud, but rather low-level, aged adulteration under variable supply chain conditions. Most literature uses binary classification to differentiate between genuine and adulterated honey, without considering the influence of low-level adulterants on multi-class botanical discrimination models.

3. Multi-Platform Stability: Comparative Strengths and Blind Spots

Different analytical platforms target different chemical domains. These domains show different perturbations in the supply chain's stability. GC-MS targets volatile compounds, which are thermally unstable. LC-MS/MS is used to analyze non-volatile metabolites, whose responses vary depending on compound type. ICP-MS measures trace elements, which resist thermal processing but shift under syrup adulteration. Rapid spectroscopic methods capture bulk profiles with high classification capability but limited chemical interpretability. Because no single chemical domain is uniformly robust across all perturbation types, the platform performance must be assessed in accordance with the expected disturbance profile. The following subsections assess this platform-specific vulnerability landscape, which is summarised in Table 1.

Table 1: Comparative vulnerability of analytical platforms to supply-chain perturbations in honey authentication

Analytical Platform	Target Marker	Thermal Processing	Filtration / Ultrafiltration	Syrup Adulteration
GC-MS	Volatile compounds associated with floral origin and aroma-linked composition	VULNERABLE Volatile loss; furan generation; thermal-history confounding [19], [6]	DATA GAP UF-specific evidence limited; indirect matrix effects [10], [4]	VARIABLE Volatile dilution; some process volatiles increase [6]
LC-MS/MS	Non-volatile: Phenolics, flavonoids, glycosides, Amadori compounds, organic acids, and related small molecules	VARIABLE Marker-specific effects; some fingerprints retained [7], [20]	VULNERABLE Selective marker depletion; classification partly preserved [11], [21]	STRONG Targeted markers; fingerprint discrimination [22], [16]
ICP-MS / ICP-OES	Trace elements and elemental ratios	STRONG Elemental stability; processing-robust reference [9]	VARIABLE Some mineral loss; UF-specific evidence limited [9]	VULNERABLE Elemental-ratio distortion; dilution-sensitive response [13]
NIR / ATR-FTIR / UV-Vis (Spectroscopic Methods)	Bulk molecular absorption profiles. water, sugar, protein bands	DATA GAP Limited direct evidence; possible spectral drift [18]	DATA GAP Limited direct evidence	STRONG Rapid screening; chemometric dependence; time-sensitive performance [23], [24]

Note. Ratings summarise the current literature at the platform level and are intended as a comparative synthesis rather than an exhaustive inventory of all reported markers. STRONG indicates that marker integrity or authentication performance is relatively preserved under the stated perturbation. VARIABLE indicates mixed, marker-class-specific, or study-dependent effects. VULNERABLE indicates marker alteration or reduced authentication reliability under the perturbation. DATA GAP indicates that direct evidence is limited or indirect inference only. Evidence for filtration and ultrafiltration is less extensive, and some judgments are informed by filtration-related studies rather than by ultrafiltration-only studies.

3.1 GC-MS

GC-MS primarily interrogates the volatile fraction of honey, capturing terpenes, aldehydes, esters, and carbonyl compounds that correlate with floral origin and aroma-linked composition. These analytes carry useful botanical information but are among the most labile in the honey matrix.

Heating mānuka honey at 90 ℃ significantly attenuated methylglyoxal (MGO) and 2'-methoxyacetophenone (MAP) [19]. In long-term storage, most endogenous volatiles decline, while newly formed furan derivatives accumulate [6].

Syrup adulteration produces a mixed volatile response. Increasing HFCS concentration dilutes most endogenous volatiles, yet some compounds, such as furfural and acetonitrile, are elevated in adulterated samples [6]. SIMCA has demonstrated the capacity to resolve adulteration from stored volatile profiles, although the discrimination depends on carefully curated reference datasets.

Therefore, GC-MS is highly sensitive to compositional change. Whilst this characteristic supports floral-origin screening, it limits the platform's value as a standalone authentication anchor when there are variables in the heat treatment history or storage conditions.

3.2 LC-MS/MS

LC-MS/MS covers the broadest non-volatile chemical space in honey authentication, comprising phenolics, flavonoids, glycosides, Amadori compounds, organic acids, and proteins.

Its thermal response is compound-class-specific. The thermal stability of flavonoids is higher than that of phenolic acids [7], and the Amadori compound Fru-Phe was found to exceed 10 mg/kg in artificially honeyfied acacia honey and less than 1.54 mg/kg in naturally matured honey, implying its use as a thermal indicator [8]. Escriche et al. [20] showed that industrial thermal treatment produced fewer effects on the phenolic profiles of Spanish honeys than year-of-collection variability and that botanical classification was not lost. This shows that LC-MS/MS botanical models can tolerate moderate thermal perturbation when the marker set is sufficiently diverse.

Filtration and ultrafiltration pose a different risk. Standard processing did not compromise the botanical classification of blueberry, canola, and clover honeys by LC-MS fingerprinting, but individual markers, such as adenosine, were selectively removed [21].

In the adulteration domain, LC-MS/MS-based approaches have demonstrated strong discriminatory capacity. HPLC-UV fingerprinting coupled with PLS-DA achieved 100% classification of various sugar syrups, with a detection limit of 15% [22]. LC-HRMS metabolomics identified a syrup-specific marker at m/z 515.1444 with a quantification limit around 5% [16].

Therefore, LC-MS/MS is a versatile platform, but its robustness is not automatic. Whether a given model withstands perturbation depends on whether the specific marker classes it relies upon survive the expected perturbation profile.

3.3 ICP-MS

ICP-MS and ICP-OES measure trace-element signatures, including K, Na, Fe, Mg, Zn, and Ca. Because minerals are thermally inert, elemental profiles remain unaffected by heating. Czipa et al. [9] demonstrated that neither thermal processing nor year of collection altered the elemental composition of acacia honey. Thus, Trace elements occupy a fundamentally different stability domain from volatiles or phenolics. This thermal resilience positions elemental profiling as a processing-robust reference layer within multi-platform authentication schemes.

By contrast, syrup adulteration severely distorts elemental profiles. The K/Na ratio decreased by over 90% at 50% adulteration and was already detectable at 10%, with the magnitude of disturbance varying by adulterant type [13]. PCA and HCA applied to elemental data cleanly separated natural from adulterated samples [13].

Filtration also affects mineral content. Czipa et al. [9] found that centrifugation and standard filtration reduced mineral levels in acacia honey, though the loss of minerals under ultrafiltration is not properly quantified.

A further limitation is that elemental signatures do not encode floral biochemistry as do volatile terpenes or phenolic profiles. Elemental profiling thus provides a robust reference for processing procedures; it can complement platforms based on organic markers, though on its own, it cannot resolve botanical origin with the specificity that chromatographic methods offer.

3.4 Rapid Spectroscopic Methods

Near-infrared (NIR), attenuated total reflectance Fourier-transform infrared (ATR-FTIR), and ultraviolet-visible (UV-Vis) spectroscopy offer rapid, lower-cost alternatives to chromatographic and elemental platforms. Rather than resolving individual metabolites, these methods capture bulk molecular absorption profiles across water, sugar, and protein bands.

For the detection of adulteration, spectroscopic approaches have reported high classification accuracy. NIR and ATR-FTIR data fusion with support vector machine (SVM) optimization, achieving 100% accuracy, sensitivity, and specificity at a detection limit of 10% syrup adulteration [23]. UV-Vis spectroscopy coupled with artificial neural networks reached 98.9% accuracy at a comparable threshold [24]. NIR-based aquaphotomics has also proven effective for identifying adulteration of manuka honey [25].

However, these results depend heavily on the chemometric model architecture and the training set composition, and their apparent performance may be time-sensitive. During post-adulteration storage, the discrimination gradually diminishes [18].

Because spectroscopic methods operate on composite absorption features, their chemical interpretability is substantially lower than that of LC-MS/MS or GC-MS. Their speed and cost advantages are best leveraged as front-end screening tools or as fusion components within multi-platform strategies, where the chemical resolution of chromatographic and elemental methods compensates for the limited molecular specificity of spectral data.

The analysis above demonstrates that no single analytical platform maintains uniform robustness across all supply-chain perturbations. Each platform contributes distinct information, and each carries a distinct vulnerability profile. We argue that robustness in honey authentication is not a property of any individual instrument but a multi-platform validation problem, one that requires systematic stress-testing protocols, external validation strategies, and data-fusion architectures.

4. Minimum Evidence Standard: Stress Testing and Validation Framework

High classification accuracy under controlled conditions does not, in itself, demonstrate that an authentication model will perform reliably across the supply chain. The perturbation evidence reviewed in Sections 2 and 3 shows that marker stability and platform performance both shift under processing and fraud scenarios. We propose, on this basis, that future authentication claims for non-mānuka honeys should meet a minimum evidence standard that goes beyond single-condition validation.

4.1 Perturbation-Aware Stress Testing

Most existing authentication studies validate models by sampling under a single set of conditions, often unperturbed, or subjected to only one perturbation type. The high classification rates reported in such settings may reflect best-case performance, rather than supply-chain robustness. Heating, filtration, and adulteration can co-occur in commercial practice.

A minimum stress-testing framework should include at least three tiers of challenge. At the first tier, heating, ultrafiltration, and syrup adulteration each need to be applied independently to establish single-factor vulnerability profiles. The second tier introduces interaction stresses, combining at least two perturbation types, such as heat with adulteration or ultrafiltration with adulteration, to evaluate whether compounded stresses amplify marker loss or generate confounding artifacts. The third tier addresses the temporal dimension. The discriminatory power of adulteration markers decays within months of the perturbation event, indicating that post-perturbation storage must be treated as a test variable in its own right [18]. Table 2 outlines a proposed sentinel framework structured along these three tiers.

Table 2: Proposed Sentinel Stress-Testing Framework for Multi-Platform Honey Authentication

Block	Stress Condition	Primary / Complementary Readout	Theoretical rationale	Observed marker response	Minimum Validation Endpoints	Evidence Basis
I. Single-Factor Baselines	Control No heating / filtration / adulteration	GC-MS + LC-MS/MS + ICP-MS (all required)	Distinguish perturbation effects from natural variation	Profiles vary by floral origin, geography, and harvest year.	Inter-batch CV by marker class; class-wise baseline separation	Direct [9], [20]
	Mild heat 50 - 55 °C	GC-MS + LC-MS/MS	Early drift before overt quality loss	TPC reduced; thermal markers (HMF / Fru-Phe) increase	Thermal-marker vs control; Feature retention	Direct [7], [8]
	Moderate heat 70 - 90 °C	GC-MS + LC-MS/MS ICP-MS (orthogonal control)	Volatile models fail; elemental models stable	Heating alters volatile/terpenoid markers; elemental profiles unaffected by heat	External-validation false-negative rate; thermal-history separation; elemental stability	Direct [9], [26]
	Filtration / ultrafiltration	LC-MS/MS + ICP-MS (optional melissopalynology)	UF-sensitive markers lost; plausible profile retained	Pollen/phenolic depletion; minerals partially reduced	Marker recovery; feature count; accuracy drop	Limited direct [9], [11], [21]
	Low adulteration Rice syrup 5 - 10 % w/w	LC-MS/MS + ICP-MS; optional spectroscopy	Threshold-region inconsistency	Targeted markers detectable; elemental-ratio shift	LOD/LOQ; balanced accuracy; class-wise sensitivity	Direct [15], [16]
II. Interaction Stress	Heat × Adulteration	LC-MS/MS + ICP-MS	Heat masks weak fraud signals	No direct study. Single-factor data: heat degrades volatiles, adulteration dilutes compositional signal	False-negative rate for adulterated samples; external-validation accuracy; fusion gain vs. best single platform	Indirect Inferred from [9], [13], [19]
	UF × Adulteration	LC-MS/MS + ICP-MS	Feature pool shrinks after UF	No direct study. UF depletes markers; adulteration shifts elemental ratios.	Detection rate after UF; retained discriminatory features; confusion matrix by adulterant level	Indirect Inferred from[11], [13], [21]
	Heat × UF	GC-MS + LC-MS/MS	Compounded feature attrition	No direct study. volatile drift and non-volatile loss	Accuracy drop; retained discriminatory features	Inferred from [11], [19]
III. Robustness Challenge	Sentinel multi-stress condition (heat + UF + adulteration)	Multi-block fusion required: GC-MS + LC-MS/MS + ICP-MS	Fusion required under worst-case stress	No direct study. full-stress evidence absent	Macro-F1 under external validation; adulterated-sample false-negative rate; fusion benefit	Proposed [27], [28], [29]

Block	Stress Condition	Primary / Complementary Readout	Theoretical rationale	Observed marker response	Minimum Validation Endpoints	Evidence Basis
	Post-perturbation storage	Spectroscopy or LC-MS/MS + ICP-MS	Fresh-sample validation overestimates robustness	Time-dependent signal decay	vs best single platform. Performance decay curve; marker-panel stability; validity window	Direct [6], [18]

Note: Syrup-type effect: All adulteration conditions above use rice syrup to isolate the concentration effect. To disentangle the syrup-type effect, an additional panel should test multiple syrup types (HFCS, beet, golden, maple) at a fixed concentration. Surrogate-system note: Most evidence cited derives from acacia, rape, manuka, and honeydew honeys. Direct validation on NZ non-mānuka honeys is absent. Transferability of these findings should not be assumed and constitutes a primary research gap.

4.2 Mandatory External Validation

Internal cross-validation is the common performance metric in honey authentication studies, but it systematically overestimates generalisability [28]. When training and test samples originate from the same batch, harvest season, or experimental condition, the resulting accuracy reflects within-study consistency, rather than real-world transferability. Honey authentication is prone to this bias because floral source, season, processing history, and perturbation profile each introduce domain shifts that internal data partitioning cannot capture.

External validation needs to address at least three levels of independence. First, models should be tested on samples from an independent harvest year or batch. Second, perturbation conditions applied to the validation set should differ from those used during training. Third, the validation set should include concentrations not represented in the training data. Where resources permit, validation across independent laboratories or regional sample sets provides further assurance against site-specific confounding.

What external validation determines, ultimately, is whether a model possesses the supply-chain transferability required for regulatory or commercial deployment. Without it, even high reported accuracy offers limited grounds for confidence.

4.3 Multi-Block Data Fusion

Each analytical platform carries a distinct vulnerability profile, and no single platform provides complete resilience across all perturbation types. Data fusion addresses this limitation: when one marker domain is degraded by a specific perturbation, an independent platform interrogating a different chemical space can provide compensatory information.

Several of the strongest performances reported in the reviewed literature relied on multi-source strategies. Include NIR and mid-infrared spectral fusion [23] and elemental profiling combined with physicochemical chemometrics [13]. Hong et al. [29] applied mid-level fusion of organic metabolic fingerprints with ICP-MS elemental profiles to seafood provenance determination and achieved high accuracy, suggesting a transferable framework for honey.

Architectures such as multi-block partial least squares appear especially suitable because they preserve the interpretability of individual data blocks while exploiting cross-platform redundancy. The goal is perturbation-aware redundancy, ensuring that when one marker domain is degraded, complementary domains compensate rather than pursuing maximal model complexity.

Future honey authentication research should shift its emphasis from marker discovery toward robustness-oriented validation. The stress-testing, external validation, and data-fusion requirements outlined above define a minimum evidence standard against which practical authentication claims for monofloral honeys can be assessed.

5. Conclusion

This review establishes that the core challenge for honey authentication beyond mānuka is not marker identification but marker survival. The evidence in Sections 2 and 3 shows that every major perturbation encountered in the supply chain, including thermal processing, membrane filtration, syrup adulteration, and post-perturbation storage, alters the chemical basis on which authentication models depend, and no single analytical platform is exempt from at least one category of vulnerability.

The Sentinel Stress-Testing Framework proposed here defines a minimum-evidence standard for future honey authentication claims by integrating three requirements: perturbation-aware challenge tiers, mandatory external validation across independent sample sets, and multi-block data fusion to exploit complementary marker domains.

For New Zealand, the framework offers a pathway toward extending the regulatory credibility already established for mānuka to non-mānuka monofloral honeys such as rewarewa and kāmahi. As the EU moves toward harmonized adulteration detection methods under Directive 2024/1438, the tiered stress-testing structure provides a transferable template for any jurisdiction seeking to anchor authenticity standards in perturbation-realistic evidence.

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Conflicts of Interest

The authors declare no conflict of interest.

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